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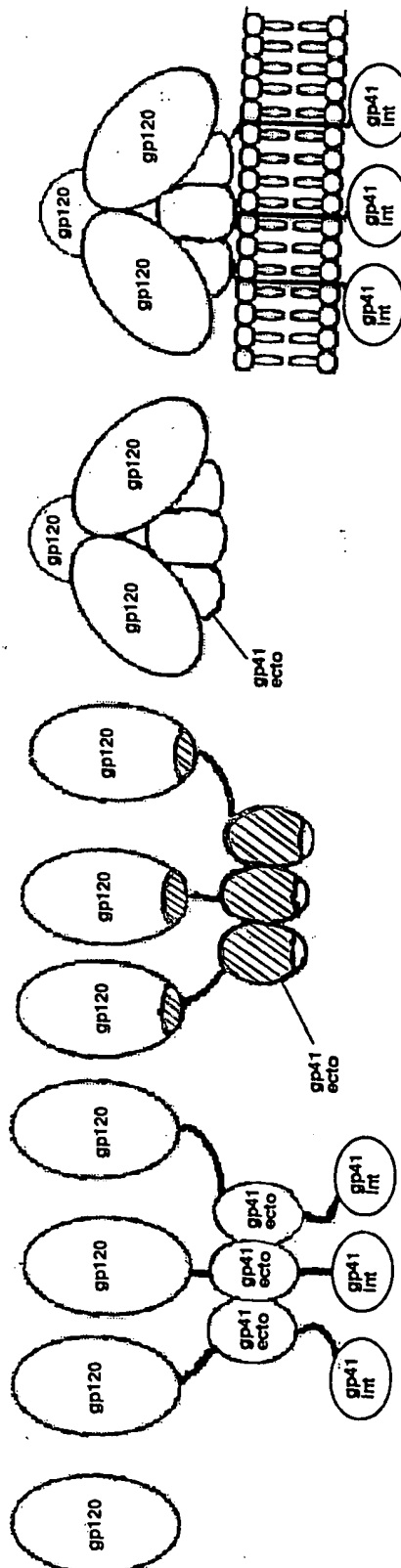
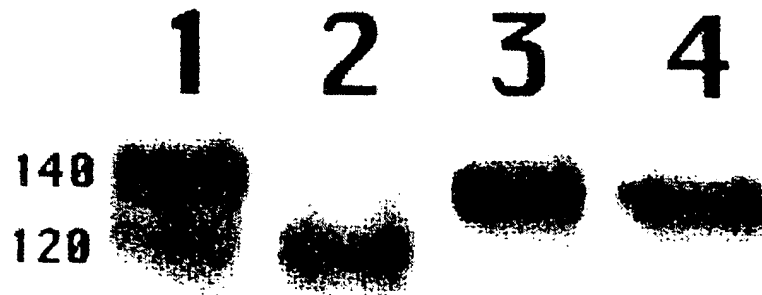


FIGURE 1

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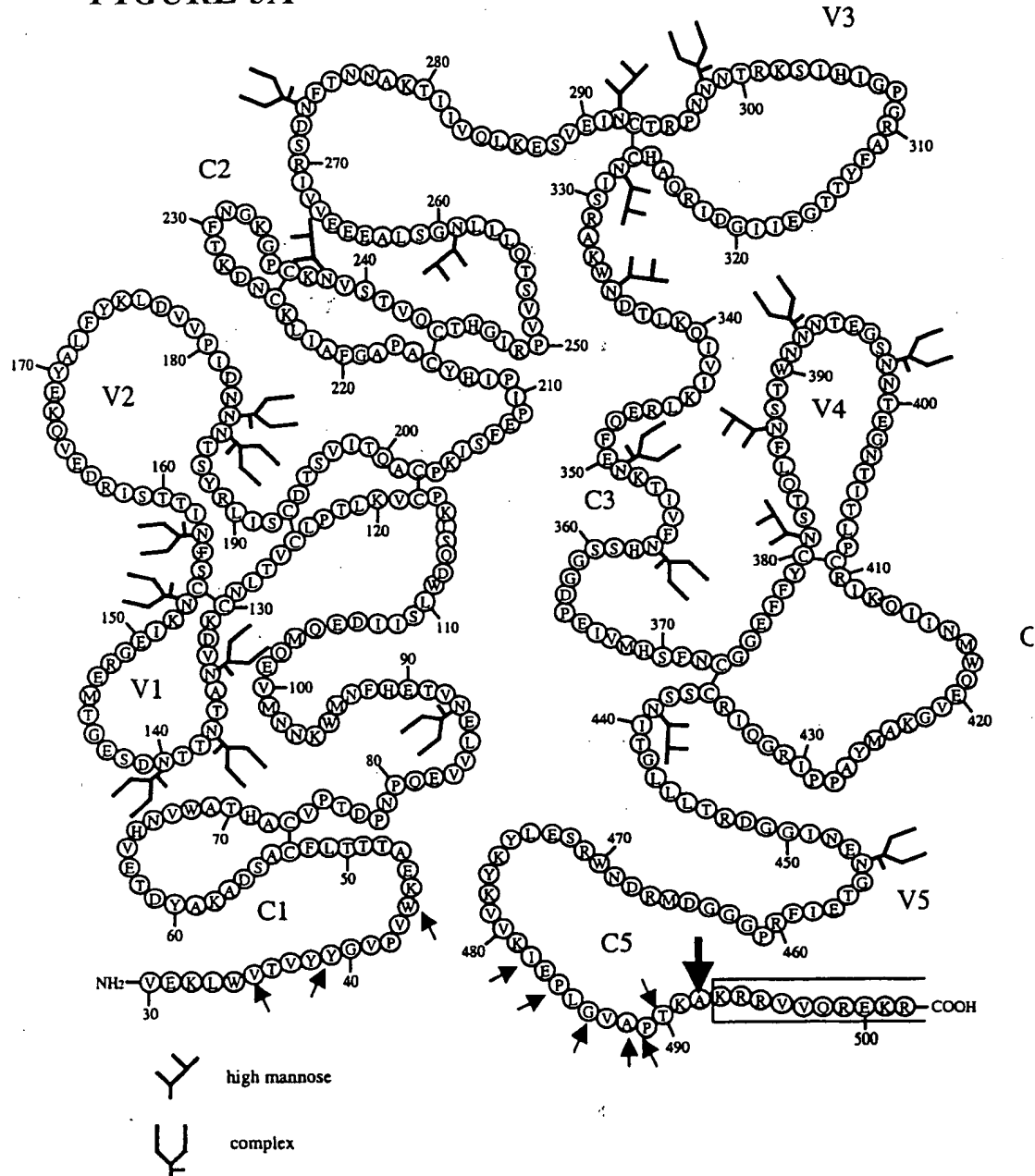
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FIGURE 2



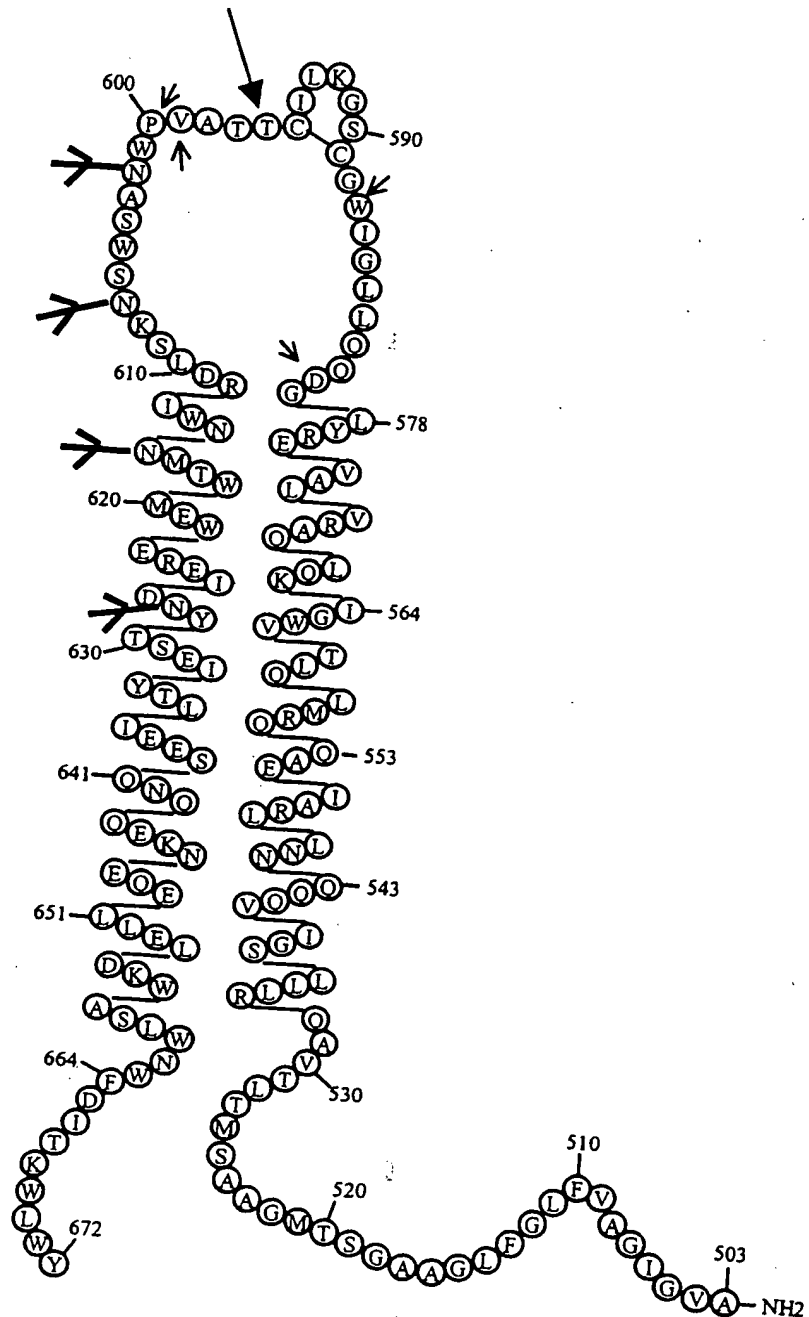
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FIGURE 3A



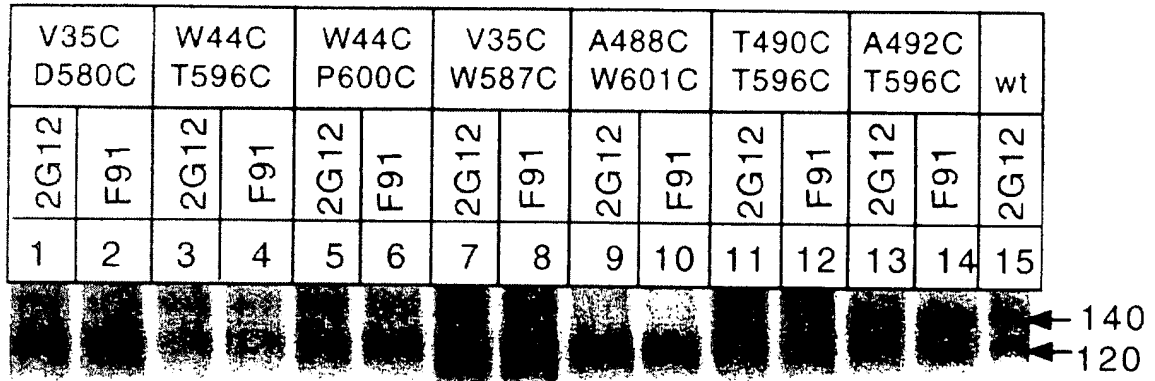
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FIGURE 3B



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FIGURE 4



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FIGURE 5

gp41						gp120	
	D580C	W587C	T596C	V599C	P600C	W601C	C1
V35C	0.45	0.40	0.35	0.30	0.40	0.30	
Y39C	0.35	0.30	0.60	0.45	0.45	N.D.	
W44C	0.45	0.45	0.65	0.50	0.65	0.45	

gp120						C5	
	D580C	W587C	T596C	V599C	P600C	W601C	C5
P484C	0.35	0.30	0.45	0	0	0	
G486C	0	0	0.25	0.20	0.30	0	
A488C	0	0	0.05	0	0	0	
P489C	0	0.10	0.30	0.15	0.05	0	
T490C	0	0.15	0.55	0.25	0.25	0.10	
A492C	0.05	0	0.75	0.50	0.10	0.25	

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FIGURE 6A

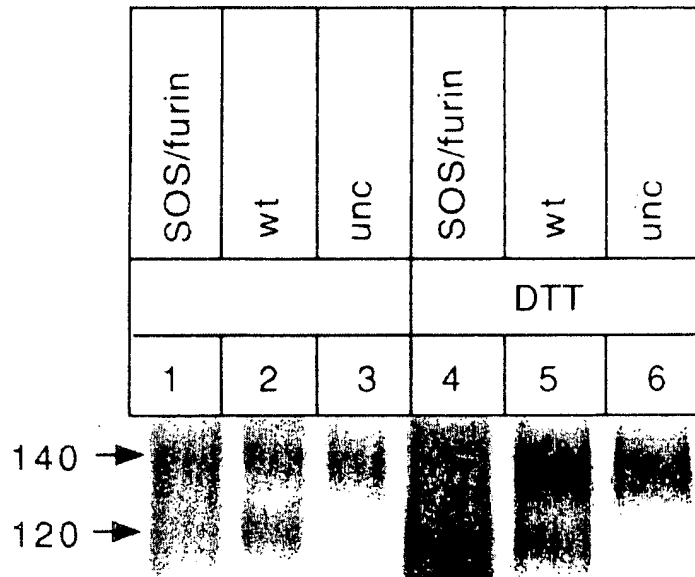


FIGURE 6B

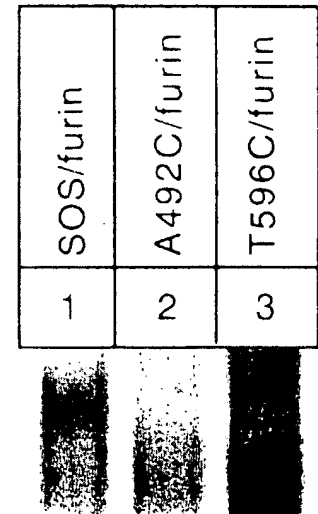
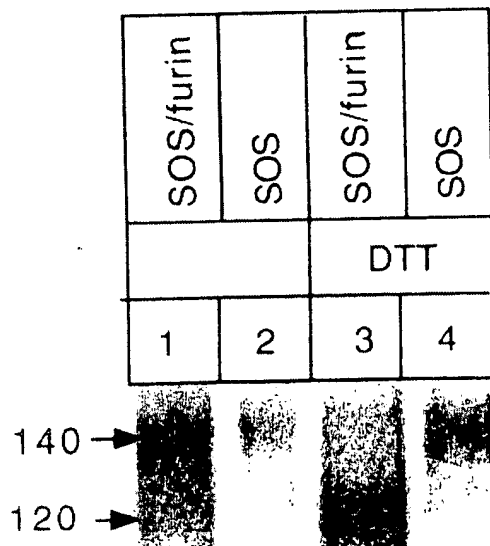
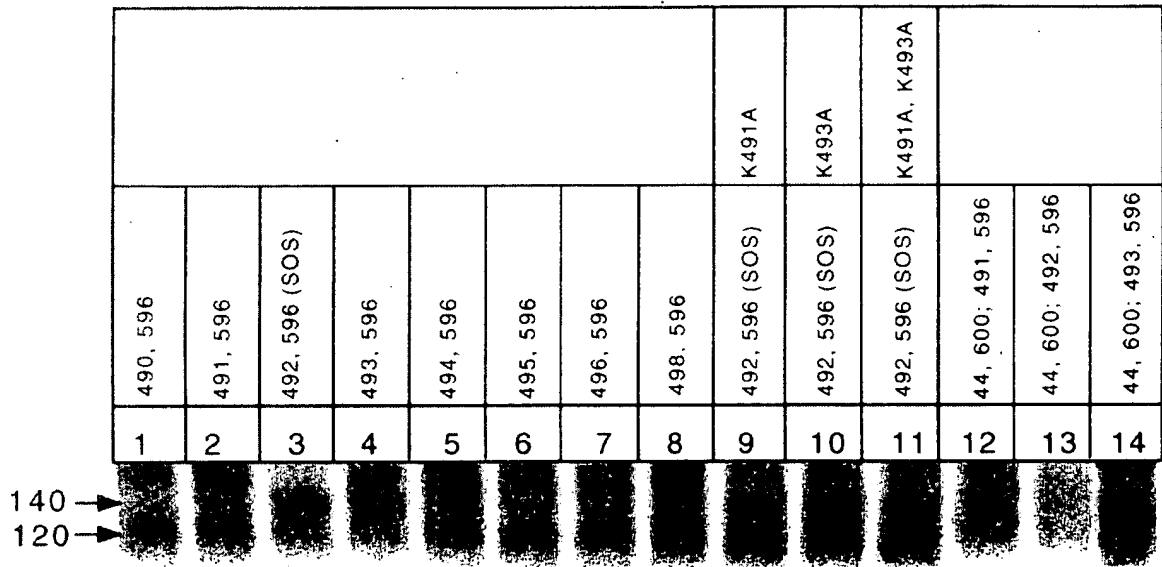


FIGURE 6C



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FIGURE 7



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FIGURE 8A

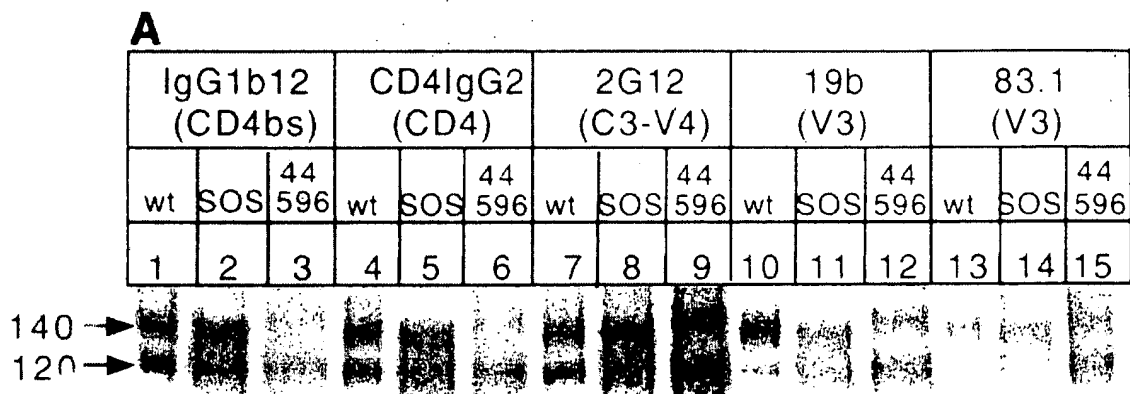


FIGURE 8B

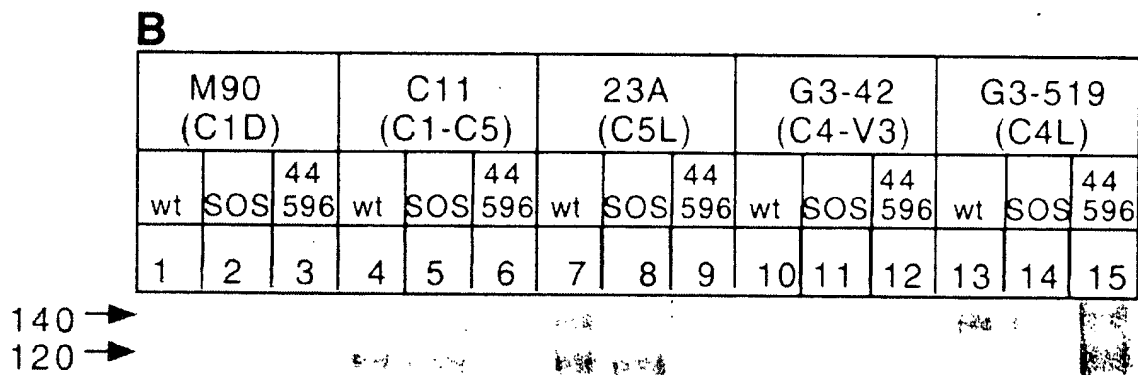
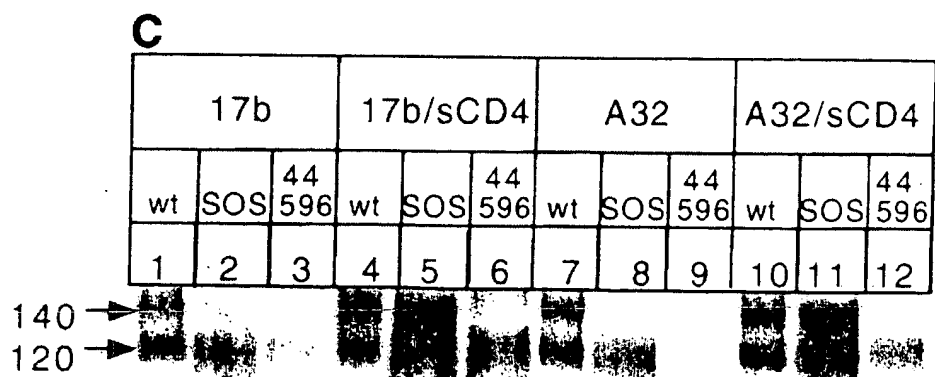


FIGURE 8C



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FIGURE 8D

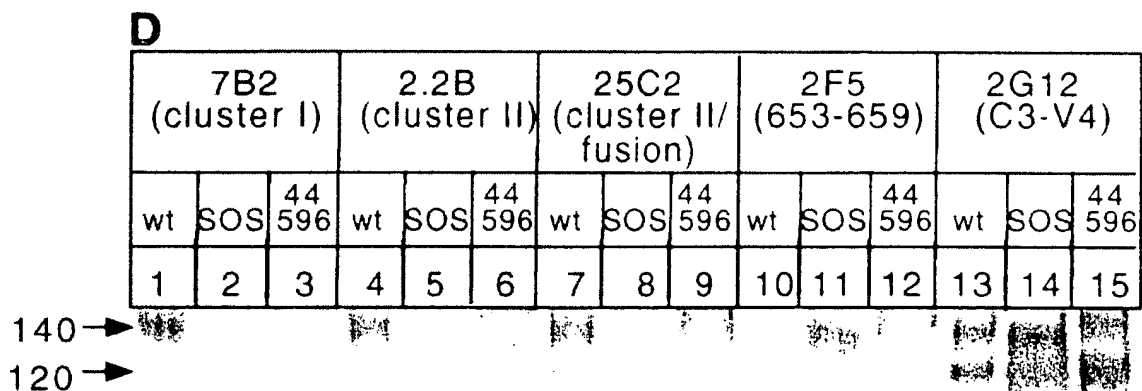
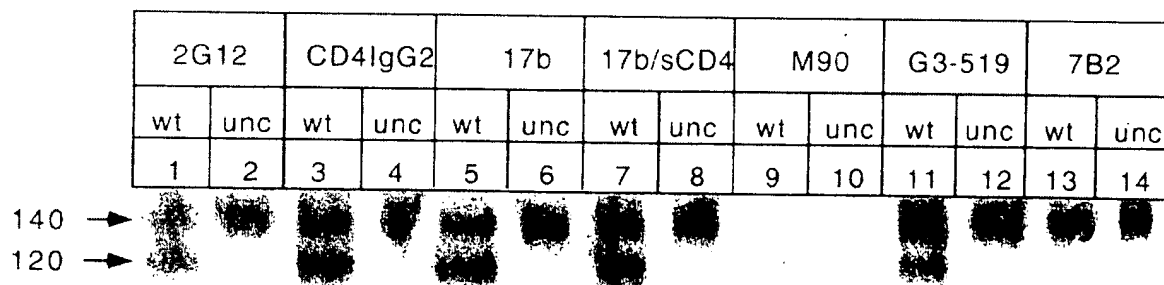


FIGURE 8E



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FIGURE 9A

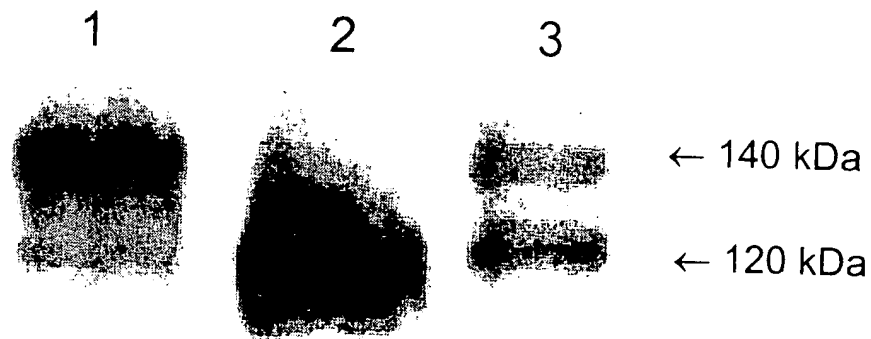


FIGURE 9B

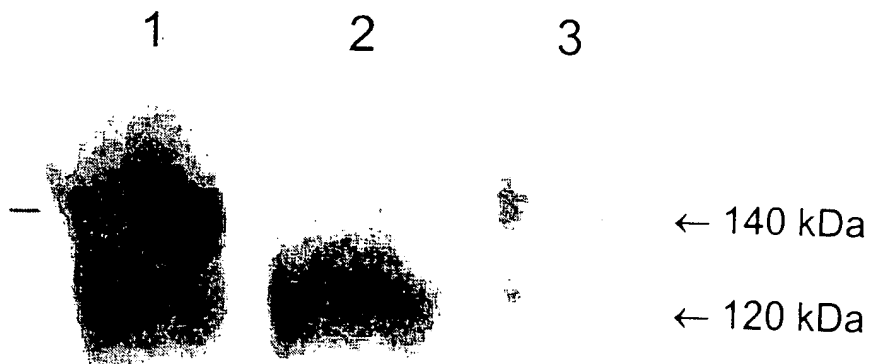
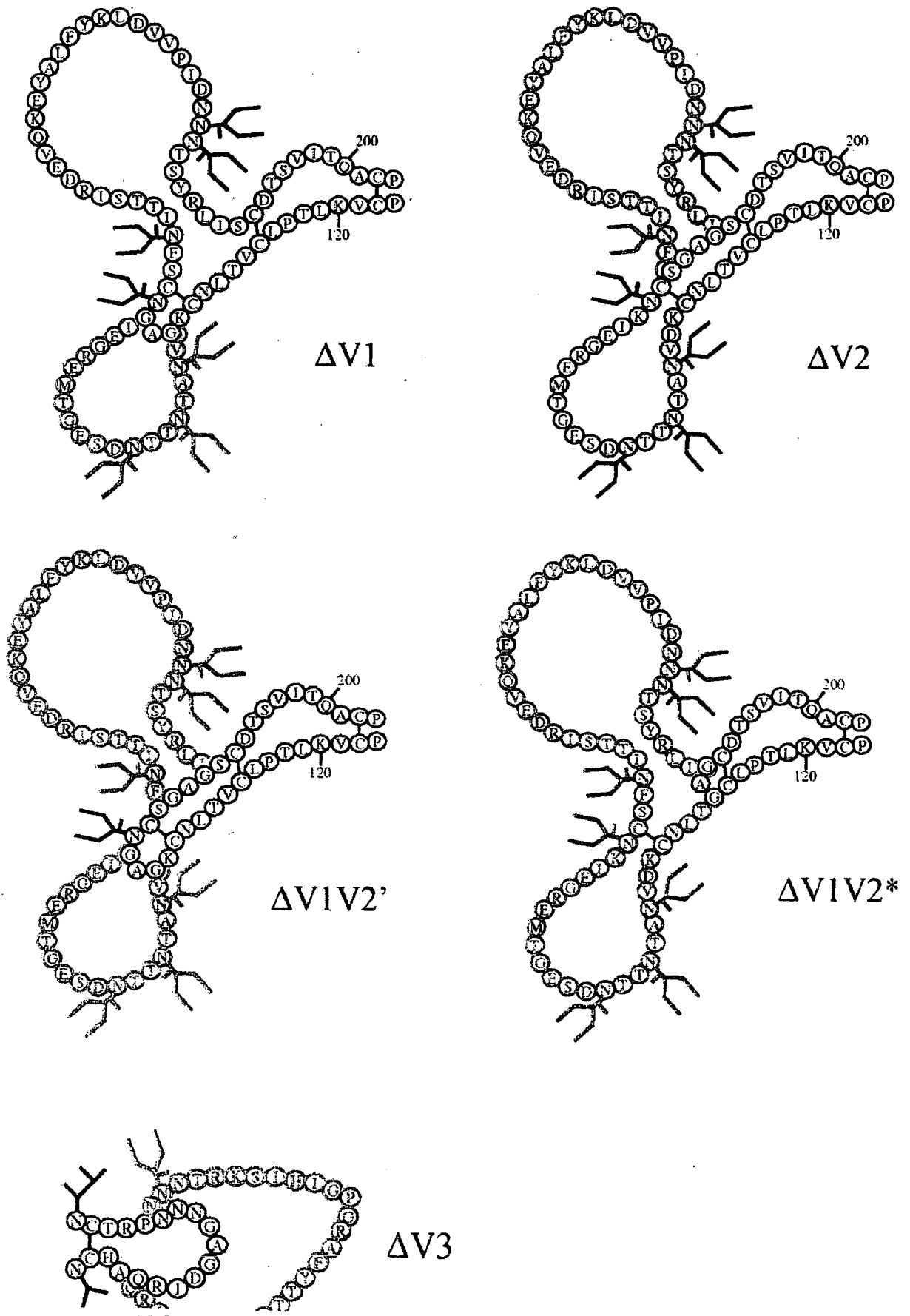


FIGURE 10

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FIGURE 11A

A

wt ΔV1V2*V3		CC ΔV1V2*V3		wt ΔV1V2*V3 N357Q N398Q		CC ΔV1V2*V3 N357Q N398Q		wt		envelope protein
2G12	F91	2G12	F91	2G12	F91	2G12	F91	F91	F91	antibody
1	2	3	4	5	6	7	8	9	10	lane

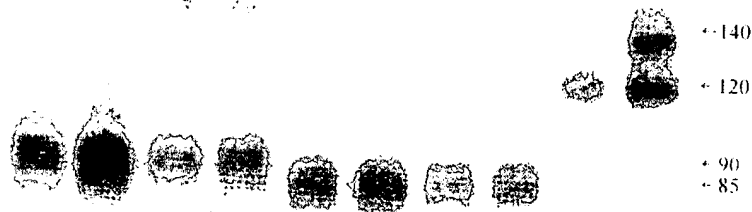
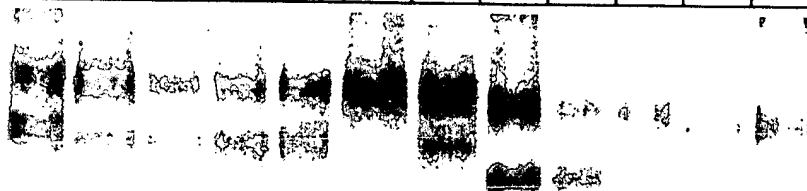


FIGURE 11B

B

wt	ΔV1		ΔV2		ΔV3		ΔV1V2'		ΔV1V2*		ΔV1V2*V3		protein
CC		CC		CC		CC		CC		CC		CC	cysteines
1	2	3	4	5	6	7	8	9	10	11	12	13	lane



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FIGURE 12A

A

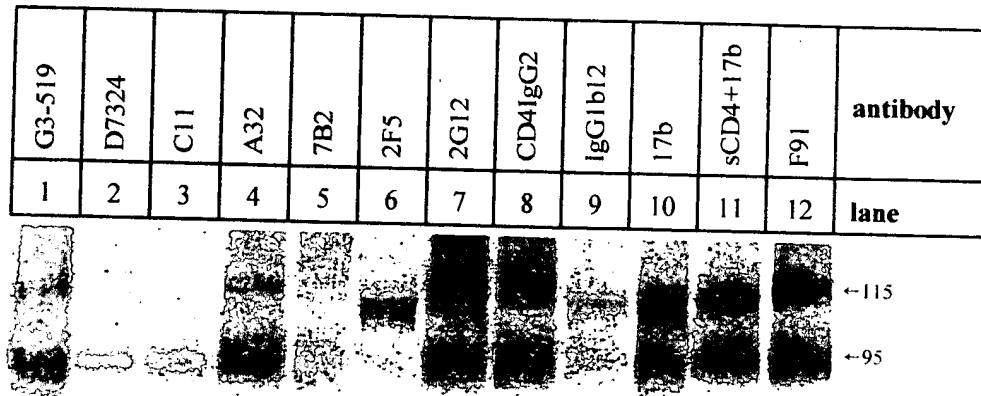
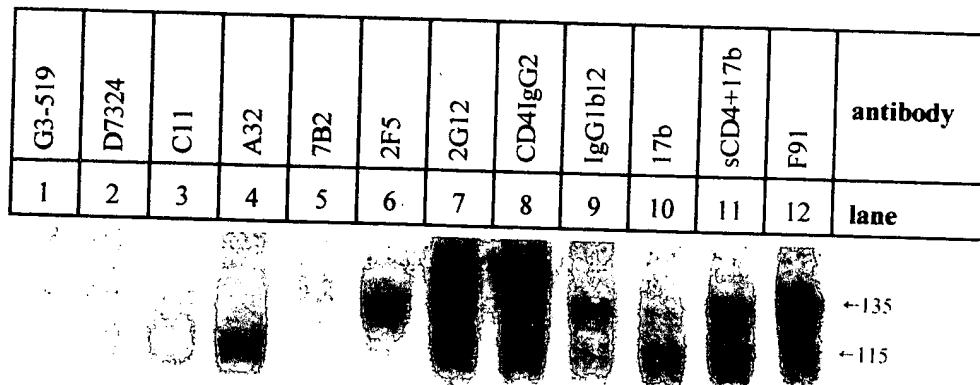


FIGURE 12B

B





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FIGURE 13A

HIV-1_{JR-FL} SOS gp140

(a)

```
1      GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51     AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101    AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151    CCACAAGAAGTAGTATTGGAAAATGTAACAGAACATTTTAACATGTGGAA
201    AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251    AAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAAT
301    TGCAAGGATGTGAATGCTACTAATACCACTAATGATAGCGAGGGAACGAT
351    GGAGAGAGGAGAAATAAAAACTGCTCTTTCAATATCACCACAAGCATAA
401    GAGATGAGGTGCAGAAAGAATATGCTCTTTTTTATAAACTTGATGTAGTA
451    CCAATAGATAATAATAATACCAGCTATAGGTTGATAAGTTGTGACACCTC
501    AGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAATTCCCATAC
551    ATTATTGTGCCCCGGCTGGTTTTGCGATTCTAAAGTGTAATGATAAGACG
601    TTCAATGGAAAAGGACCATGTAAAAATGTCAGCACAGTACAATGTACACA
651    TGGAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGGCAGTCTAG
701    CAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACAATGCTAAA
751    ACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGTACAAGACC
801    CAACAACAATACAAGAAAAAGTATACATATAGGACCAGGGAGAGCATTTT
851    ATACTACAGGAGAAATAATAGGAGATATAAGACAAGCACATTGTAACATT
901    AGTAGAGCAAAATGGAATGACACTTTAAACAGATAGTTATAAAATTAAG
951    AGAACAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGG
1001   ACCCAGAAATTGTAATGCACAGTTTTAATTGTGAAGGAGAATTTTCTAC
1051   TGTAATTCAACACAACCTGTTTAATAGTACTTGGAATAATAACTGAAGG
1101   GTCAAATAACACTGAAGGAAATACTATCACACTCCCATGCAGAATAAAAC
1151   AAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCC
1201   ATCAGAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTGCTATTAAC
1251   AAGAGATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAGACCTGGAG
1301   GAGGAGATATGAGGGACAATTGGAGAAGTGAATTCTATAAATATAAGTA
1351   GTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAGAGAAGAGT
1401   GGTGCAAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCCCTGGGT
1451   TCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACACTGACG
1501   GTACAGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAGAACAATTT
1551   GCTGAGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCACAGTCTGGG
1601   GCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGATACCTAGGG
1651   GATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACCTCATTTGCTG
1701   CACTGCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCTAGATAGGA
1751   TTTGGAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTAC
1801   ACAAGCGAAATATACACACTAATTGAAGAATCGCAGAACCAACAAGAAAA
1851   GAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATT
1901   GGTTTGACATAACAACTGGCTGTGGTAT
```

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FIGURE 13B

30	VEKLWVTVYY	GVPVWKEATT	TLFCASDAKA	YDTEVHNVWA	THACVPTDPN
80	PQEVVLENT	EHFNMWKNNM	VEQMQEDIIS	LWDQSLKPCV	KLTPLCVTLN
130	CKDVNATNTT	NDSEGTMERG	EIKNCSFNIT	TSIRDEVQKE	YALFYKLDVV
180	PIDNNNTSYR	LISCDTSVIT	QACPKISFEP	IPIHYCAPAG	FAILKCNDKT
230	FNGKGPCKNV	STVQCTHGIR	PVVSTQLLLN	GSLAEEEVVI	RSDNFTNNAK
280	TIIVQLKESV	EINCTRPNNN	TRKSIHIGPG	RAFYTTEGII	GDIRQAHCNI
330	SRAKWNDTLK	QIVIKLREQF	ENKTIVFNHS	SGGDPEIVMH	SFNCEGEFFY
380	CNSTQLFNST	WNNNTEGSNN	TEGNTITLPC	RIKQIINMWQ	EVGKAMYAPP
430	IRGQIRCSSN	ITGLLLTRDG	GINENGTEIF	RPGGGDMRDN	WRSEFYKYKV
480	VKIEPLGVAP	TKCKRRVVQR	EKRAVGIGAV	FLGFLGAAGS	TMGAASMTLT
530	VQARLLLSGI	VQQQNLLRA	IEAQQRMLQL	TVWGIKQLQA	RVLAVERYLG
580	DQQLLGIWGC	SGKLICCTAV	PWNASWSNKS	LDRIWNNMTW	MEWEREIDNY
630	TSEIYTLIEE	SONQOEKNEQ	ELLELDKWAS	LWNWFEDITNW	LWY



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FIGURE 14A

HIV-1_{JR-FL} ΔV1V2* SOS gp140

(a)

```
1   GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51  AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101 AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151 CCACAAGAAGTAGTATTGGAATGTAACAGAACATTTTAACATGTGGAA
201 AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251 AAAGCCTAAAGCCATGTGTAAAATTAACCCCACTCTGTGGTGCAGGATGT
301 GACACCTCAGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAAT
351 TCCCATAACATTATTGTGCCCCGGCTGGTTTTGCGATTCTAAAGTGTAATG
401 ATAAGACGTTCAATGAAAAGGACCATGTAAAAATGTCAGCACAGTACAA
451 TGTACACATGGAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGG
501 CAGTCTAGCAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACA
551 ATGCTAAAACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGT
601 ACAAGACCCAACAACAATACAAGAAAAAGTATACATATAGGACCAGGGAG
651 AGCATTTTATACTACAGGAGAAATAATAGGAGATATAAGACAAGCACATT
701 GTAACATTAGTAGAGCAAAATGGAATGACACTTTAAACAGATAGTTATA
751 AAATTAAGAGAACAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTC
801 AGGAGGGGACCCAGAAATTGTAATGCACAGTTTTAATTGTGGAGGAGAAT
851 TTTTCTACTGTAATTC AACACA ACTGTTTAATAGTACTTGG AATAATAAT
901 ACTGAAGGGTCAAATAACACTGAAGGAAATACTATCACACTCCCATGCAG
951 AATAAAACAAATTATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATG
1001 CCCCTCCCATCAGAGGACAAATTAGATGTTTCATCAAATATTACAGGGCTG
1051 CTATTAACAAGAGATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAG
1101 ACCTGGAGGAGGAGATATGAGGGACAATTGGAGAAGTGAATTATATAAAT
1151 ATAAAGTAGTAAAAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAG
1201 AGAAGAGTGGTGCAAAGAGAAAAAGAGCAGTGGGAATAGGAGCTGTGTT
1251 CCTTGGGTTCTTGGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGA
1301 CACTGACGGTACAGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAG
1351 AACAATTTGCTGAGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCAC
1401 AGTCTGGGGCATCAAGCAGCTCCAGGCAAGAGTCCTGGCTGTGGAAAGAT
1451 ACCTAGGGGATCAACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAACTC
1501 ATTTGCTGCACTGCTGTGCCTTGGAATGCTAGTTGGAGTAATAAATCTCT
1551 GGATAGGATTTGGAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTG
1601 ACAATTACACAAGCGAAATATACACCCTAATTGAAGAATCGCAGAACCAA
1651 CAAGAAAAGAATGAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTT
1701 GTGGAATTGGTTTGACATAACAACTGGCTGTGGTAT
```



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FIGURE 14B

(b)

30	VEKLWVTVYY	GVPVWKEATT	TLFCASDAKA	YDTEVHNVWA	THACVPTDPN
80	PQEVVLENT	EHFNMWKNNM	VEQMQEDIIS	LWDQSLKPCV	KLTPLCGAGC
130	DTSVITQACP	KISFEPIPIH	YCAPAGFAIL	KCNDKTFNGK	GPCKNVSTVQ
180	CTHGIRPVVS	TQLLNGSLA	EEEVVIRSDN	FTNNAKTIIV	QLKESVEINC
230	TRPNNNTRKS	IHIGPGRAFY	TTGEIIGDIR	QAHCNISRAK	WNDTLKQIVI
280	KLREQFENKT	IVFNHSSGGD	PEIVMHSFNC	GGEFFYCNST	QLFNSTWNNN
330	TEGSNNTEGN	TITLPCRIKQ	IINMWQEVGK	AMYAPPPIRGQ	IRCSSNITGL
380	LLTRDGGINE	NGTEIFRPGG	GDMRDNRWSE	LYKYKVVKIE	PLGVAPTKCK
430	RRVVQREKRA	VGIGAVFLGF	LGAAGSTMGA	ASMTLTVQAR	LLLSGIVQQQ
480	NNLLRAIEAQ	QRMLQLTVWG	IKQLQARVLA	VERYLGDQQL	LGIWGC SGKL
530	ICCTAVPWNA	SWSNKSLDRI	WNNMTWMEWE	REIDNYTSEI	YTLIEESQNO
580	QEKNEQELLE	LDKWASLWNW	FDITNWLWY		



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FIGURE 15A

HIV-1_{JR-FL} ΔV3 SOS gp140

(a)

```
1      GTAGAAAAGTTGTGGGTCACAGTCTATTATGGGGTACCTGTGTGGAAAGA
51     AGCAACCACCACTCTATTTTGTGCATCAGATGCTAAAGCATATGATACAG
101    AGGTACATAATGTTTGGGCCACACATGCCTGTGTACCCACAGACCCCAAC
151    CCACAAGAAGTAGTATTGGAAAATGTAACAGAACATTTTAACATGTGGAA
201    AAATAACATGGTAGAACAGATGCAGGAGGATATAATCAGTTTATGGGATC
251    AAAGCCTAAAGCCATGTGTAAATTAACCCCACTCTGTGTTACTTTAAAT
301    TGCAAGGATGTGAATGCTACTAATAACCACTAATGATAGCGAGGGAACGAT
351    GGAGAGAGGAGAAAATAAAAACTGCTCTTTCAATATCACCACAAGCATAA
401    GAGATGAGGTGCAGAAAGAATATGCTCTTTTTTATAAACTTGATGTAGTA
451    CCNATAGATAATAATAATACCAGCTATAGGTTGATAAGTTGTGACACCTC
501    AGTCATTACACAGGCCTGTCCAAAGATATCCTTTGAGCCAATTCCCATAC
551    ATTATTGTGCCCCGGCTGGTTTTTGCATTCTAAAGTGTAATGATAAGACG
601    TTCAATGGAAAAGNCCATGTAAAAATGTCAGCACAGTNCAATGTACACA
651    TGGAATTAGGCCAGTAGTATCAACTCAACTGCTGCTAAATGGCAGTCTAG
701    CAGAAGAAGAGGTAGTAATTAGATCTGACAATTTACGAACAATGCTAAA
751    ACCATAATAGTACAGCTGAAAGAATCTGTAGAAATTAATTGTACAAGACC
801    CAACAACAATGGAGCCGGCGATATAAGACAAGCACATTGTAACATTAGTA
851    GAGCAAAATGGAATGACACTTTAAAACAGATAGTTATAAAATTAAGAGAA
901    CAATTTGAGAATAAAACAATAGTCTTTAATCACTCCTCAGGAGGGGACCC
951    AGAAATTGTAATGCACAGTTTTAATTGTGGAGGAGAATTTTTTCTACTGTA
1001   ATTCAACACAACCTGTTTAATAGTACTTGGAATAATAATACTGAAGGGTCA
1051   AATAACACTGAAGGAAATACTATCACACTCCCATGCAGAATAAAACAAAT
1101   TATAAACATGTGGCAGGAAGTAGGAAAAGCAATGTATGCCCTCCCATCA
1151   GAGGACAAATTAGATGTTTATCAATATTACAGGGCTGCTATTAACAAGA
1201   GATGGTGGTATTAATGAGAATGGGACCGAGATCTTCAGACCTGGAGGAGG
1251   AGATATGAGGGACAATTGGAGAAAGTGAATTATATAAATATAAAGTAGTAA
1301   AAATTGAACCATTAGGAGTAGCACCCACCAAGTGCAAGAGAAGAGTGGTG
1351   CAAAGAGAAAAAAGAGCAGTGGGAATAGGAGCTGTGTTCTTGGGTTCTT
1401   GGGAGCAGCAGGAAGCACTATGGGCGCAGCGTCAATGACACTGACGGTAC
1451   AGGCCAGACTATTATTGTCTGGTATAGTGCAACAGCAGAACAAATTTGCTG
1501   AGGGCTATTGAGGCGCAACAGCGTATGTTGCAACTCACAGTCTGGGGCAT
1551   CAAGCAGCTCCAGGCAAGAGTCTGGCTGTGGAAAGATACCTAGGGGATC
1601   AACAGCTCCTGGGGATTTGGGGTTGCTCTGGAAAACCTCATTTGCTGCACT
1651   GCTGTGCCCTTGAATGCTAGTTGGAGTAATAAATCTCTGGATAGGATTTG
1701   GAATAACATGACCTGGATGGAGTGGGAAAGAGAAATTGACAATTACACAA
1751   GCGAAATATACACCCTAATTGAAGAATCGCAGAACCAACAAGAAAAGAAT
1801   GAACAAGAATTATTGGAATTAGATAAATGGGCAAGTTTGTGGAATTGGTT
1851   TGACATAACAAAATGGCTGTGGTAT
```



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FIGURE 15B

30	VEKLWVTVYY	GVPVWKEATT	TLFCASDAKA	YDTEVHNVWA	THACVPTDPN
80	PQEVVLENT	EHFNMWKNNM	VEQMQEDIIS	LWDQSLKPCV	KLTPLCVTLN
130	CKDVNATNTT	NDSEGTMERG	EIKNCSFNIT	TSIRDEVQKE	YALFYKLDVV
180	XIDNNNTSYR	LISCDTSVIT	QACPKISFEP	IPIHYCAPAG	FAILKCNDKT
230	FNGKXPCKNV	STXQCTHGIR	PVVSTQLLLN	GSLAEDEVVI	RSDNFTNNAK
280	TIIVQLKESV	EINCTRPNNN	GAGDIRQAHC	NISRAKWNDT	LKQIVIKLRE
330	QFENKTIVFN	HSSGGDPEIV	MHSFNCGGEF	FYCNSTQLFN	STWNNNTEGS
380	NNTEGNTITL	PCRIKQIINM	WQEVGKAMYA	PPIRGQIRCS	SNITGLLLTR
430	DGGINENGTE	IFRPGGGDMR	DNWRSELYKY	KVVKIEPLGV	APTKCKRRVV
480	QREKRAVGIG	AVFLGFLGAA	GSTMGAASMT	LTVQARLLLS	GIVQQQNNLL
530	RAIEAQQRML	QLTVWGIKQL	QARVLAVERY	LGDQQLLGIW	GCSGKLICCT
580	AVPWNASWSN	KSLDRIWNNM	TWMEWEREID	NYTSEIYTLLI	EESQNQQEKN
630	EQELLELDKW	ASLWNWFDIT	KWLWY		

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